WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Tuesday, December 21, 2004

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L1	(sequenc$ same (simultaneous$ near (both strand)))	16
☐	L2	((reaction vessel or vessel or tube or single tube or chamber) same primer)	15671
☐	L3	L2 same (dNTP or deoxynucleotide triphosphate)	2337
☐	L4	L3 same (ddNTP or dideoxynucleotide triphosphate)	113
☐	L5	L4 same (thermostable polymerase or thermal$ stable polymerase or Taq)	9
☐	L6	L5 same kit	3
☐	L7	L5 and kit	8
☐	L8	L3 and (thermostable polymerase or thermal$ stable polymerase or Taq)	1787
☐	L9	L3 same(thermostable polymerase or thermal$ stable polymerase or Taq)	1000
☐	L10	L9 same kit	129
☐	L11	L10 same (ddNTP or dideoxynucleotide triphosphate)	3
☐	L12	L10 and (ddNTP or dideoxynucleotide triphosphate)	10
☐	L13	sequenc$ near primers or sequencing primers	25336
☐	L14	L13 same (single near vessel or chamber or single tube or single carrier)	138
☐	L15	L14 same (ddNTP or dNTP)	34
☐	L16	L14 same (ddNTP and dNTP)	6
☐	L17	L16 and polymerase	6
☐	L18	L14 same thermostabl$ polymerase	1
☐	L19	l14 and kit	75
☐	L20	(multiplex near sequenc$) same (primers and polymerase)	19
☐	L21	L20 and l2	11

END OF SEARCH HISTORY

L17: Entry 6 of 6 File: USPT Nov 4, 1997

DOCUMENT-IDENTIFIER: US 5683657 A
TITLE: DNA meltometer

Brief Summary Text (6):
Over the last decade, research in human genetics has undergone enormous advances, and in over one hundred human diseases a genetic lesion has been identified associated with the disease (Antonarakis, 1989, N. Engl. J. Med. 320: 153-163). The techniques used in the discovery and characterization of these disease-associated DNA polymorphisms include: (1) in vitro amplification of specific nucleic acid sequences, particularly using the polymerase chain reaction; (2) separation and sizing of nucleic acid fragments using gel electrophoresis; (3) detection of particular nucleic acid fragments amongst a multiplicity of such fragments by specific hybridization of nucleic acid bound to various membranes (so-called "Southern" and "Northern" hybridizations); and (4) determination of nucleotide sequences by degradative or, more frequently, synthetic sequencing methods (see Sambrook et al., 1990, Molecular Cloning: A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. for a detailed description of these techniques).

Brief Summary Text (11):
The apparatus and methods provided by the invention are useful for: (a) sizing nucleic acids ranging in length from about 50 to about 500 basepairs (bps) in length; (b) quantitating an amount of a specific DNA fragment, either alone or in a mixture of heterologous DNA fragments; (c) detecting a specific nucleotide sequence of a nucleic acid among a plurality of non-specific nucleotide sequences by hybridization to a sequence-specific nucleic acid probe; and (d) detecting a nested set of extended nucleic acid sequencing oligonucleotides ranging in length from about 20 to about 100 nucleotides, each extended oligonucleotide having at its 3' extent a polymerase chain-terminating compound, thereby providing for gel-free nucleotide sequencing of nucleic acids.

Detailed Description Text (21):
Polymerase chain reactions are performed using standard techniques. A DNA sample comprising the DNA template to be amplified is mixed at a final concentration of about 10.sup.4 molecules/reaction in a reaction mixture containing a first oligonucleotide PCR primer of between 15 and 30 nucleotides, that is homologous to a DNA sequence flanking the DNA fragment to be amplified, and that is labeled at the 5' end with a tethering molecule such as biotin. Also in the reaction mixture is a second oligonucleotide PCR primer of between 15 and 30 nucleotides, that is homologous to a DNA sequence flanking the DNA fragment to be amplified, and on the strand opposite to the strand homologous to the first PCR primer, said second PCR primer being labeled at the 5' end with a fluorescent molecule such as rhodamine or fluorescein or an infrared label such as a polymethine dye. Each of the PCR primers is present in the reaction mixture at a final concentration of 1 .mu.M. The reaction mixture also contains: (1) a DNA polymerase such as the thermostable polymerase from T. aquaticus (available from Perkin Elmer-Cetus, Emeryville, Calif.) at a final concentration of 1-5U/reaction; (2) each of 4 deoxynucleotide triphosphates, at a total dNTP concentration of about 200 .mu.M; and (3) a buffer

appropriate for the polymerase enzyme used, the buffer typically containing a magnesium ion salt at a concentration of 1-5 mM.

Detailed Description Text (22):
The DNA fragment is amplified following an amplification protocol involving repeated cycles of denaturation of double-stranded DNA, annealing and polymerase-catalyzed extension of the oligonucleotide primers. Amplification is performed for between 10-40 cycles, or until approximately 50-1500 ng (100 picomole) of the DNA fragment have been produced.

Detailed Description Text (28):
Hybridization of a genetic polymorphism-specific probe with human genomic DNA is achieved as follows. DNA from an individual diagnosed as a carrier of the sickle cell anemia trait [GTG (Glu.sup.6).fwdarw.GAG (Val.sup.6) in the human .beta.-globin gene] is digested with a restriction enzyme that does not destroy the polymorphism and that produces a recessed 3' end of each restriction fragment. The DNA is then labeled with ferritin under standard conditions (see Sambrook et al., ibid.), for example, by performing a fill-in reaction of the 3' recessed end using the Klenow fragment of E. coli DNA polymerase I or T4 DMA polymerase and ferritinylated dUTP.

Detailed Description Text (33):
Dideoxynucleotide/replacement synthesis nucleic acid sequencing of a site of a genetic polymorphism is performed, and a nested set of extended oligonucleotides detected using the DNA meltometer as follows. DNA from an individual diagnosed as a carrier of the genetic polymorphism that causes cystic fibrosis (deletion of the three-base codon encoding Phe.sup.463 in the cystic fibrosis transmembrane regulator gene) is digested with a restriction enzyme that does not destroy the polymorphism and that produces a recessed 3' end of each restriction fragment. The DNA is then labeled with biotinylated dUTP by fill-in reaction of the 3' recessed end using the Klenow fragment of E. coli DNA polymerase I or T4 DNA polymerase, under standard conditions (see Sambrook et al., ibid. for details of this protocol). Alternatively, a DNA fragment encompassing the site of the genetic polymorphism is produced by in vitro amplification, for example, as described in Example 1.

Detailed Description Text (34):
The biotinylated DNA sample is then denatured and mixed with streptavidin-coated latex beads and then placed into the thermomodulating chamber of the meltometer, the chamber containing a Teflon.RTM. retaining filter. A DNA sequencing oligonucleotide primer that hybridizes to a site flanking the polymorphism in the cystic fibrosis-associated DNA fragment is then added to the thermomodulating chamber. A mixture of a DNA polymerase, the appropriate buffers and unlabeled dNTPs, and each of four differentially fluorescently- or infrared-labeled dideoxynucleotide triphosphates is then added to the thermomodulating chamber, at a temperature that allows the sequencing primer to anneal and the polymerase to incorporate dNTPs and ddNTPs into a set of extended oligonucleotides encompassing the cystic fibrosis polymorphic site. After an appropriate amount of time to allow the maximum amount of oligonucleotide extension to occur, the excess sequencing reaction mixture is flushed from the thermomodulating chamber using the pump to generate a flow of washing solution as in Example 2 above through the thermomodulating chamber and past a detector, which is calibrated to detect each of the labeled ddNTPs. Each of the control steps herein described for performance of the DNA fragment detection is preferably performed by a computer in combination with a I/O interface, and the data generated from the detector is also recorded by the computer to form a permanent record of the experiment.

Previous Doc Next Doc Go to Doc#

L15: Entry 31 of 34 File: USPT Jul 13, 1999

DOCUMENT-IDENTIFIER: US 5922591 A
TITLE: Integrated nucleic acid diagnostic device

Detailed Description Text (180):
The reactor device dimensions were as follows: channels were 250 .mu.m wide by 125 .mu.m deep; the three reaction chambers were 1.5 mm wide by 13 mm in length by 125 to 500 .mu.m deep, with the reactor volumes ranging from 2.5 to 10 .mu.l. Briefly, PCR was carried out by introducing 0.3 units of Taq polymerase, 0.2 mM dNTPs, 1.5 mM MgCl.sub.2, 0.2 .mu.M primer sequences, approximately 2000 molecules of template sequence and 1.times.Perkin-Elmer PCR buffer into the bottom chamber. The thermal cycling program included (1) an initial denaturation at 94.degree. C. for 60 seconds, (2) a denaturation step at 94.degree. C. for 20 seconds, (3) an annealing step at 65.degree. C. for 40 seconds, (4) an extension step at 72.degree. C. for 50 seconds, (5) repeated cycling through steps 2-4 35 times, and (6) a final extension step at 72.degree. C. for 60 seconds.

L15: Entry 32 of 34 File: USPT May 12, 1998

DOCUMENT-IDENTIFIER: US 5750346 A
TITLE: Host organism capture

Drawing Description Text (99):
In another embodiment of the subject method, additional biochemical analytical steps may be performed after the host cell archiving step. For example, the progeny cells may be bound to cell capture regions located on the walls of the incubation chambers 50. After the bound cells may then be lysed and the released polynucleotides bound to non-specific polynucleotide capture regions, e.g., immobilized silica particles, the bound polynucleotide may then be washed so as to remove contaminants. The sequencing chambers having the bound polynucleotides may then be archived. Alternatively, after washing, PCR amplification primers, a DNA polymerase, and other reagents necessary for PCR may be added to the incubation chambers. The incubation chambers may then be subjected to a series of thermocycles in order to amplify a DNA sequence of interest. The amplified DNA may then be bound on sequence specific polynucleotide capture regions, e.g., immobilized sequencing primers. Polynucleotide sequencing reagents such as dye-labeled terminators, dNTPs, DNA polymerase, and the like may then be added to the incubation chambers in order to provide for sequencing of the bound polynucleotide sequences of interest.

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: L10 same primer pair

Display: 50 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search | Clear | Interrupt

Search History

DATE: Tuesday, December 21, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L1	09/802110	1	L1
L2	L1 and reaction vessel	1	L2
L3	L2 and single reaction vessel	1	L3
L4	(multiple or plurality) near sequencing primers	11	L4
DB=EPAB; PLUR=YES; OP=ADJ			
L5	WO-8911211-A.did.	0	L5
DB=USPT; PLUR=YES; OP=ADJ			
L6	US-5114839-A.did.	1	L6
L7	US-5114839-A.did.	1	L7
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L8	sequencing primers	7092	L8
L9	L8 near (single reaction vessel or reaction vessel or vessel or chamber or tube or column or reaction container)	6	L9
L10	L8 same(single reaction vessel or reaction vessel or vessel or chamber or tube or column or reaction container)	349	L10

L11	L10 and primer pair	96	L11
L12	L10 same primer pair	7	L12

END OF SEARCH HISTORY

enzyme substrate derivatives, and determining the base sequence of the elongation product obtained using Matrix-assisted laser desorption/ionization time-of-flight mass spectrometer (MALI-TOM-MS) analysis; (8) determining (M5) the base sequence of a nucleic acid template comprises at least one base capable of base pairing and different from the standard W-C bases, involves providing a nucleic acid template comprising at least one base capable of base pairing and different from the standard W-C standard bases, carrying out elongation by using a **primer**, a promoter, or a promoter and initiator in the presence of nucleoside triphosphates whose base comprises at least one base capable of base pairing and different from the standard W-C bases by adding a first nucleoside triphosphate and detecting PPi release and degrading the first nucleoside triphosphate, then adding a second nucleoside triphosphate, and repeating the procedure according to the kind of base of the nucleoside triphosphates provided, repeating elongation according to the template bases number desired to be sequenced, and determining the sequence of the template as the sequence of the nucleoside triphosphates added; (9) determining (M6) the base sequence of a nucleic acid template comprises at least one base capable of base pairing and different from the standard W-C bases, involves providing a number of oligonucleotides fixed on a chip, where the oligonucleotides comprises at least one base capable of base pairing and different from the standard W-C bases and having overlapping frames displaced by one or two bases, hybridizing the oligonucleotides with a labeled template according to the invention comprising at least one base capable of base pairing and different from the standard W-C bases, detecting the signal of the label, and determining the sequence of the template as the set of overlapping oligonucleotides that are labeled; (10) a compound 2',3'-dideoxyisoguanosine 5'-trisphosphate (ddisoG) (V) or 2',3'-dideoxyisocytidine 5'-trisphosphate (ddisoC) (VI); (11) preparing (V), involves preparing the N-oxide of ddATP by precipitation of a mixture of disodium salt of ddATP and a solution of monopermaleic acid, purifying the prepared N-oxide of ddATP and irradiating the purified N-oxide of ddATP with light from a high pressure mercury arc lamp, and recovering the final product ddisoG; and (12) preparing (VI), involves preparing 2',3'-deoxyisocytidine from a mixture of 2,5'-anhydro-2',3'-dideoxyuridine and methanol, adding a solution of triethylammonium bicarbonate to 2',3'-deoxyisocytidine and removing the solvent by evaporation, purifying the product obtained above by HPLC, and recovering 2',3'-deoxyisocytidine 5'-triphosphate.

BIOTECHNOLOGY - Preparation: The aptamers were prepared using standard recombinant techniques. Preferred Aptamer: (I) is a single, double or triple stranded nucleic acid, DNA, RNA or PNA. The number of bases of the aptamer is 1-300. Preferred Method: In M1, the aptamers comprises at least one standard W-C base A, C, G, T or U and at least one base capable of base pairing and different from the standard W-C bases. The base capable of base pairing and different from the W-C standard bases is selected from iso-C, iso-G, 2,6-diaminopyrimidine, xanthine, 6-amino-5-substituted pyrazin-2(1H)-one, 1-methyl-pyrazolo(4.3-d)pyrimidine-5,7(4H,6H)-dione, 5-aza-7-deazaguanine, 6-amino-3-substituted pyrazin-2(1H)-one, 3-amino-1-methylpurin-2-one, 2,4-diamino-5,6-dihydropyryimidine, 2-amino-6-(N,N-dimethylamino)purine, pyridin-2-one, 3-methyl isocarbostyril, 5-methyl isocarbostyril, 7-propynyl isocarbostyril, m-xylene, 1,3,4-trimethylbenzene, 2-methylanaphthalene, 1,4-dimethylnaphthalene, 1-methylanaphthalene, naphthalene, 7-azaindole, isocarbostyril, 6-methyl-7-azaindole, 3-propynyl-7-azaindole, imidazopyridine, pyrrolopyridine, or a heterocyclic base of formula (a)-(p). R = the point of attachment of the base to position 1 of a ribose or deoxyribose ring; X = nitrogen atom or carbon atom bearing a substituent Z; Z = hydrogen, an unfunctionalized lower alkyl chain, or a lower alkyl chain bearing an amino, carboxyl, hydroxyl, thiol, aryl, indole, or imidazolyl group; Y = N or CH, and each ring contains no more than three nitrogen consecutively bonded. In M1, the base capable of base pairing and different from the standard W-C

bases is isoC and/or isoG. In M1, the amplification is performed by polymerase chain reaction (PCR) and where the base triphosphates different from W-C bases have a different concentration from the concentration of the standard W-C base triphosphates or a base different from standard W-C bases is isoC and/or isoG and the concentration of isoC and isoG triphosphates is lower than the concentration of the standard W-C base bases triphosphates. The ligand is selected from amino acids, peptides, proteins, lipids, oligosaccharides, alkaloids, terpenes, co-enzymes, antibiotics, and their derivatives and complexes, preferably protein or modified protein. The molecular weight of the ligand is less than 5000 daltons. In M2, the template is DNA or RNA, the synthesizing enzyme is DNA- or RNA-dependent DNA or RNA polymerase, the synthesizing enzyme substrate is a number of dNTPs or NTPs and substrate derivatives comprise ddNTPs or 3'-dNTPs derivatives. A **dNTP** or a **ddNTP**, or NTP or 3'-dNTPs derivative are labeled. **Primer** or initiator is labeled. The label is an isotope, a chromophore, or a fluorophore. Preferred Substrate: In (II), the aptamer is fixed to the substrate by a spacer sequence. (II) comprises a number of aptamers that specifically bind to particular known ligands. (II) is a chip substrate. Preferred **Kit**: (III) comprises one or more labels for labeling a pool of ligands.

USE - (I) is useful for isolating a specific ligand from a pool of ligands, involves providing at least one specific aptamer, mixing (I) with a pool of ligands, and recovering the specific ligand bound to specific aptamer. (I) is useful for detection of specific ligand from a biological sample, by selecting at least one specific aptamer, capable of binding to a specific ligand from a biological sample, mixing the at least one specific aptamer with a biological sample to allow binding of the ligand to the at least one aptamer, and detecting the presence and/or quantity of the specific ligand from the biological sample bound to at least one aptamer (all claimed). (I) is useful as a drug and for therapeutic treatment.

EXAMPLE - Template 1 of 81 nucleotides comprising the aptamer of GCGTAACGGGGTCTATGTTCCCGCACACCGTGGCAAAACT was selected, sequenced and amplified with a **primer** having TGTAAAACGACGGCCAGT and a **primer** 5'-TGCCATTTCATTACCTCTTTCTCCGCACCCGACATAGATGACACTACTAC GGTATGATCCTATGGAGAACGCTCAGCGGATAACAATTTCACAC-3' which comprised the recognition site of Pl-SceI, a spacer of 50 bp 5'-GCACCCGACATAGATGACATAGATGACACTACTACGGTATGATCCTATGGAGAACGCTC-3', and the annealing site to single stranded DNA 5'-AGGGGATAACAATTTCACAC-3' and in the standard condition except for the concentrations of isoG and isoC which were 100 microM. After polymerase chain reaction, the obtained dsDNA comprising the aptamer was incubated with Pl-SceI to create an overhanging 3' end. (56 pages)

L7 ANSWER 12 OF 15 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2001-06921 BIOTECHDS
TITLE: Species-specific detection of organisms, particularly for identifying bacteria causing sepsis, comprises amplification and elongation of ribosomal nucleic acid; the use of polymerase chain reaction
AUTHOR: Krupp G; Scheinert P; Soeller R; Spengler U
PATENT ASSIGNEE: Artus-Soc.Diagn.Hamburg
LOCATION: Hamburg, Germany.
PATENT INFO: WO 2001007648 1 Feb 2001
APPLICATION INFO: WO 1999-EP5234 22 Jul 1999
PRIORITY INFO: DE 1999-5234 22 Jul 1999
DOCUMENT TYPE: Patent
LANGUAGE: German
OTHER SOURCE: WPI: 2001-168568 [17]
AN 2001-06921 BIOTECHDS
AB A method for detecting species-specific of prokaryotic and eukaryotic organisms is claimed. It involves performing DNA (e.g. ribosome DNA or rRNA spacer region) amplification. Amplification is by any standard

method and many sequencing **primer** (SP), each with a different marker, are used, with the elongation reaction being done in the presence of **dideoxynucleotide triphosphate** (**dNTP**) as a chain break. Also claimed are processing or concentrating bacteria by lysis of non-bacterial cell then centrifuging to produce a bacterial pellet; isolating or enriching bacterial DNA by lysing bacteria in the pellet; kits for performing methods; a **kit** for performing the new detection process. The method is especially used to detect sepsis causing bacteria in blood, protozoon (flagellates, ameba or ciliates) in blood, Salmonella sp. in meat, and fish in spawn. Other application include detecting contaminants in food, seed etc., detecting helminths, or fungal pathogens (in humans, animals or plants), identification of varieties, races etc. in animal and plant breeding, investigation of biodiversity, and detection of infectious agents in a wide range of tissues. (46pp)

L7 ANSWER 13 OF 15 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2001-10134 BIOTECHDS
TITLE: Composition for detecting microorganisms, comprising deoxynucleotide triphosphates, **dideoxynucleotide triphosphate**, and thermostable polymerase to incorporate **dideoxynucleotide triphosphate** into extending polymer;
DNA **primer** for Chlamydia trachomatis, HIV virus and human papilloma virus detection or serotyping and infection diagnosis
AUTHOR: Leushner J; Hui M; Dunn J M; LaCroix J M
PATENT ASSIGNEE: Visible-Genetics
LOCATION: Toronto, Ontario, Canada.
PATENT INFO: US 6214555 10 Apr 2001
APPLICATION INFO: US 1999-311260 13 May 1999
PRIORITY INFO: US 1999-311260 13 May 1999
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-289718 [30]
AN 2001-10134 BIOTECHDS
AB A composition (I) containing a mixture of four deoxynucleotide triphosphates (dNTPs) and at least one **dideoxynucleotide triphosphate** (**ddNTP**) corresponding to one of the four dNTPs, at a molar ratio of 1:50 to 1:500, and a thermally stable polymerase enzyme (II) which incorporates **ddNTP** into an extending DNA polymer at a rate not less than 0.4-fold the rate of incorporation of dNTPs, is claimed. Also claimed is a **kit** for detecting a target microorganism containing, in packaged combination, a pair of DNA **primers** which bind to the sense and antisense strands, respectively, and flank a secreted region within the genome target microorganism, a mixture of four dNTPs and at least one **ddNTP**, at a molar ration of 1:50 to 1:1,000, and (II). (I) and the **kit** are useful for detecting a target microorganism e.g. Chlamydia trachomatis, HIV virus and human papilloma virus. The method follows a simple test format which is generally applicable to the detection of microorganisms, including infectious disease-causing microorganisms, and particularly for a simple test which provides an indication of the specific nature, e.g. the serotype or the organism. (62pp)

L7 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:397088 CAPLUS
DOCUMENT NUMBER: 135:15067
TITLE: DNA sequencing method which employs various DNA polymerases and **kit** used for the same
INVENTOR(S): Park, Hanoh; You, Jaehyung
PATENT ASSIGNEE(S): Bioneer Corporation, S. Korea
SOURCE: PCT Int. Appl., 26 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001038574	A1	20010531	WO 2000-KR1354	20001125
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
KR 2001051853	A	20010625	KR 2000-69269	20001121
EP 1144689	A1	20011017	EP 2000-981879	20001125
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001178500	A2	20010703	JP 2000-359455	20001127

PRIORITY APPLN. INFO.:
KR 1999-52889 A 19991126
KR 2000-69269 A 20001121
WO 2000-KR1354 W 20001125

AB The present invention relates to a DNA nucleotide sequence anal. method by means of using dideoxy nucleotide-mediated chain termination reaction and to a **kit** used for the same, and more particularly, directed to a DNA nucleotide sequence anal. method using various DNA polymerases of which affinities to dideoxynucleotide are different from each other. A mixture of the conventional DNA polymerase (Top DNA polymerase), Tfi mutant DNA polymerase, and Thermo Sequenase was used to sequence pUC plasmid DNA.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 15 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
ACCESSION NUMBER: 1996-15150 BIOTECHDS
TITLE: Cosmid vector for introducing defects into macromolecular DNA ;
phage lambda-based vector for DNA mutagenesis
PATENT ASSIGNEE: Toyobo
LOCATION: Japan.
PATENT INFO: JP 08214881 27 Aug 1996
APPLICATION INFO: JP 1996-28240 16 Feb 1996
PRIORITY INFO: JP 1995-28240 16 Feb 1995
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
OTHER SOURCE: WPI: 1996-436936 [44]
AN 1996-15150 BIOTECHDS
AB A new cosmid vector comprises a phage lambda cos sequence, at least 2 different drug-resistance genes, at least 2 replication origins, an RNA-polymerase transcription initiation sequence and a multi-cloning site. Also new are: stepwise introduction of defects into macromolecular DNA in an in vitro DNA packaging system using the new cosmid vector; and the in vitro DNA packaging system, which comprises a composition of a factor prepared from a phage for packaging DNA into phage particles and the cosmid vector. The system is used for packaging DNA into phage particles and the packaging reaction is terminated successively for stepwise introduction of mutations into DNA. A **kit** for structural determination of DNA using the new system and containing DNA-polymerase, DNA-ligase and a DNA **primer**, **dNTP** and **ddNTP** is also new. DNA is packaged stepwise as DNA fragments with mutations into phage particles and then extracted. The nucleotide sequence of each DNA fragment with a mutation is determined and the

respective determined sequences are combined to determine the whole sequence of the DNA. (11pp)